

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/532,423  
Source: IFWO  
Date Processed by STIC: 10/6/06

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 10/06/2006

PATENT APPLICATION: US/10/532,423

TIME: 10:09:14

Input Set : A:\2006-09-28 4600-0112PUS1.txt

Output Set: N:\CRF4\10062006\J532423.raw

3 <110> APPLICANT: Keietsu ABE et al.  
 5 <120> TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF USEFUL PRODUCTS BY MEANS OF  
 6 DECOMPOSITION OF PLASTICS BY MICROORGANISMS  
 8 <130> FILE REFERENCE: 4600-0112PUS1  
 10 <140> CURRENT APPLICATION NUMBER: US 10/532,423  
 11 <141> CURRENT FILING DATE: 2005-04-22  
 13 <150> PRIOR APPLICATION NUMBER: PCT/JP03/11861  
 14 <151> PRIOR FILING DATE: 2003-09-17  
 16 <150> PRIOR APPLICATION NUMBER: JP 2002-30884  
 17 <151> PRIOR FILING DATE: 2002-10-23  
 19 <150> PRIOR APPLICATION NUMBER: JP 2002-371246  
 20 <151> PRIOR FILING DATE: 2002-12-24  
 22 <160> NUMBER OF SEQ ID NOS: 46  
 24 <170> SOFTWARE: PatentIn version 3.1  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 497  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Aspergillus oryzae  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: CDS  
 33 <222> LOCATION: (1)..(453)  
 35 <400> SEQUENCE: 1

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 37 Met Gln Phe Ser Val Ala Ala Val Leu Ala Leu Ala Thr Ala Val Ala  
 38 1 5 10 15  
 40 gct ctt cct cct gcc tct ggc act ggc gct ggc cag caa gtc gga cac 96  
 41 Ala Leu Pro Pro Ala Ser Gly Thr Gly Ala Gly Gln Gln Val Gly His  
 42 20 25 30  
 44 tcc aag aac gac ttc cct ctc cct aag gag ttg acc acc aag cag gcc 144  
 45 Ser Lys Asn Asp Phe Pro Leu Pro Lys Glu Leu Thr Thr Lys Gln Ala  
 46 35 40 45  
 48 gcc gac aag tgt ggt gac cag gct cag ctc acc tgc tgc aac aag acc 192  
 49 Ala Asp Lys Cys Gly Asp Gln Ala Gln Leu Thr Cys Cys Asn Lys Thr  
 50 50 55 60  
 52 gtc aag acc ggt gac ttc acc cag gtt gag gag ggt ctc ctt gct ggc 240  
 53 Val Lys Thr Gly Asp Phe Thr Gln Val Glu Glu Gly Leu Leu Ala Gly  
 54 65 70 75 80  
 56 ctc ctc tcc aac ctc ctc ggt gcc gga cag ggc tcc cag ggt ctt ggt 288  
 57 Leu Leu Ser Asn Leu Leu Gly Ala Gly Gln Gly Ser Gln Gly Leu Gly  
 58 85 90 95  
 60 ctc ttg gat gag tgc acc aac atc cct gtt atc ccc atc atc tcc atc 336  
 61 Leu Leu Asp Glu Cys Thr Asn Ile Pro Val Ile Pro Ile Ser Ile  
 62 100 105 110

*see p. 6*

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64 gcc tct cct cag gag aag tgc aag cag ccc atc tct tgc tgc cag aac      384
65 Ala Ser Pro Gln Glu Lys Cys Lys Gln Pro Ile Ser Cys Cys Gln Asn
66      115      120      125
68 acc aag tcc agc gcc gat ggc gac ctc gtc ggt att ggt ctt cct tgc      432
69 Thr Lys Ser Ser Ala Asp Gly Asp Leu Val Gly Ile Gly Leu Pro Cys
70      130      135      140
72 atc gct ctc ggc tct ctc ctg taagcgattg cattcgcgaa aatggttagct      483
73 Ile Ala Leu Gly Ser Leu Leu
74 145      150
76 cgaggagcac ggga      497
80 <210> SEQ ID NO: 2
81 <211> LENGTH: 438
82 <212> TYPE: DNA
83 <213> ORGANISM: Aspergillus oryzae
85 <220> FEATURE:
86 <221> NAME/KEY: CDS
87 <222> LOCATION: (1)..(438)
89 <400> SEQUENCE: 2
90 atg aag ttc ttc gct gtc gct gct ctc ttc gcc acc gcc gcc atg gcc      48
91 Met Lys Phe Phe Ala Val Ala Ala Leu Phe Ala Thr Ala Ala Met Ala
92 1      5      10      15
94 gct cct ggt tcc gct cct gtg ccc ggt gct gct gct gct gcc ggc aac      96
95 Ala Pro Gly Ser Ala Pro Val Pro Gly Ala Ala Ala Ala Ala Gly Asn
96      20      25      30
98 ggt aac gcc ccg gtt atc aac cag acc cag cag aag gcc ttc aca gac      144
99 Gly Asn Ala Pro Val Ile Asn Gln Thr Gln Gln Lys Ala Phe Thr Asp
100      35      40      45
102 gct tgc agt gct aag ggc aac cac ccc gtc tgc tgc gac cag atc gac      192
103 Ala Cys Ser Ala Lys Gly Asn His Pro Val Cys Cys Asp Gln Ile Asp
104      50      55      60
106 acc tcc aag acc aca act gtg aac gag gga ctt ctc ggt ggc ctc ctc      240
107 Thr Ser Lys Thr Thr Val Asn Glu Gly Leu Leu Gly Gly Leu Leu
108 65      70      75      80
110 ggt gag ggc ctg ggt ggc gtt ctt aac aac ctt gtt ggt ggc gag cct      288
111 Gly Glu Gly Leu Gly Gly Val Leu Asn Asn Leu Val Gly Gly Glu Pro
112      85      90      95
114 ggc gct tgc agt ggt ctt gtt tct gcc ctc aac aag caa tgc cag acc      336
115 Gly Ala Cys Ser Gly Leu Val Ser Ala Leu Asn Lys Gln Cys Gln Thr
116      100      105      110
118 agc atc ggt tgc tgc cag cag aac gcc aag ggc gac aac tac cag agc      384
119 Ser Ile Gly Cys Cys Gln Gln Asn Ala Lys Gly Asp Asn Tyr Gln Ser
120      115      120      125
122 ggc ctc ctc aac ctc aac ctc cag gct cct tgc ctt ctc agc aat ggt      432
123 Gly Leu Leu Asn Leu Asn Leu Gln Ala Pro Cys Leu Leu Ser Asn Gly
124      130      135      140
126 ctg taa      438
127 Leu
128 145
131 <210> SEQ ID NO: 3

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132 <211> LENGTH: 318
133 <212> TYPE: DNA
134 <213> ORGANISM: Aspergillus oryzae
136 <220> FEATURE:
137 <221> NAME/KEY: CDS
138 <222> LOCATION: (1)..(318)
140 <400> SEQUENCE: 3
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143 1          5          10          15
145 agt tgc gcg gat cca acc gca caa tgc gat aac gga ccc gtt caa tgc      96
146 Ser Ser Ala Asp Pro Thr Ala Gln Cys Asp Asn Gly Pro Val Gln Cys
147          20          25          30
149 tgc gca acg gtc ggt tta ccg act gac agt gta gtc tca cct tta ctt     144
150 Cys Ala Thr Val Gly Leu Pro Thr Asp Ser Val Val Ser Pro Leu Leu
151          35          40          45
153 ggc ttg ctc gga gta gtt gtt cca gac atg agc act cca gtt gga ttg     192
154 Gly Leu Leu Gly Val Val Pro Asp Met Ser Thr Pro Val Gly Leu
155          50          55          60
157 acc tgt aat cct att gtc cag ggt gga tct tgc cca ggc cac ccc gtt     240
158 Thr Cys Asn Pro Ile Val Gln Gly Gly Ser Cys Pro Gly His Pro Val
159 65          70          75          80
161 tgc tgt aca gga aat gta ggc cat gct tct gcg aca cat tgt tcc agc     288
162 Cys Cys Thr Gly Asn Val Gly His Ala Ser Ala Thr His Cys Ser Ser
163          85          90          95
165 tac cta atg tcc atc gga aat gat tac tga      318
166 Tyr Leu Met Ser Ile Gly Asn Asp Tyr
167          100          105
170 <210> SEQ ID NO: 4
171 <211> LENGTH: 675
172 <212> TYPE: DNA
173 <213> ORGANISM: Aspergillus oryzae
175 <220> FEATURE:
176 <221> NAME/KEY: CDS
177 <222> LOCATION: (1)..(675)
179 <400> SEQUENCE: 4
180 atg gtg atg ctc cgc tcc ctc ctc gtc tct gcc ctg gct gct ctg gca      48
181 Met Val Met Leu Arg Ser Leu Leu Val Ser Ala Leu Ala Ala Leu Ala
182 1          5          10          15
184 gca ggc agc ccc atc gct gag cca gcg gac cag tca ctg gaa gcc aga      96
185 Ala Gly Ser Pro Ile Ala Glu Pro Ala Asp Gln Ser Leu Glu Ala Arg
186          20          25          30
188 cag ctc ggg tct tcc aat gac ctc acc aac ggt gca tgc aag gat gtg     144
189 Gln Leu Gly Ser Ser Asn Asp Leu Thr Asn Gly Ala Cys Lys Asp Val
190          35          40          45
192 acc ctc att ttc gct cga ggc tcc acc gaa atg ggc aac atg ggc act     192
193 Thr Leu Ile Phe Ala Arg Gly Ser Thr Glu Met Gly Asn Met Gly Thr
194          50          55          60
196 gtc atc gga ccc cct ctc tgc tcg tcg ctg aag agc aag ctc ggt gcc     240

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197 Val Ile Gly Pro Pro Leu Cys Ser Ser Leu Lys Ser Lys Leu Gly Ala
198 65                               70                               75                               80
200 gac aag gtc gct tgc caa ggt gtg ggt ggc ttg tac aca gga gga ttg      288
201 Asp Lys Val Ala Cys Gln Gly Val Gly Gly Leu Tyr Thr Gly Gly Leu
202                               85                               90                               95
204 atg caa aat gct ctc cct cag aac acc gac ccc ggc gct atc tcc acc      336
205 Met Gln Asn Ala Leu Pro Gln Asn Thr Asp Pro Gly Ala Ile Ser Thr
206                               100                              105                              110
208 gcg aag tcg ctc ttt gaa caa gcc agc acc aag tgc cct aac acc cag      384
209 Ala Lys Ser Leu Phe Glu Gln Ala Ser Thr Lys Cys Pro Asn Thr Gln
210                               115                              120                              125
212 atc gtg gcc ggt gga tac agt caa ggt agt gcc gtc atc gac aac gcc      432
213 Ile Val Ala Gly Gly Tyr Ser Gln Gly Ser Ala Val Ile Asp Asn Ala
214                               130                              135                              140
216 gtc caa caa ctc tcc gcc gaa gtc aag gac aag gtc aag ggt gtt gtt      480
217 Val Gln Gln Leu Ser Ala Glu Val Lys Asp Lys Val Lys Gly Val Val
218 145                               150                              155                              160
220 ttc ttc ggc ttc act cgt aac ctc cag gac aag ggt cag atc ccc aac      528
221 Phe Phe Gly Phe Thr Arg Asn Leu Gln Asp Lys Gly Gln Ile Pro Asn
222                               165                              170                              175
224 tac ccc aag gac aat gtt aag gtc ttt tgt gcg atg gga gat ctt gtc      576
225 Tyr Pro Lys Asp Asn Val Lys Val Phe Cys Ala Met Gly Asp Leu Val
226                               180                              185                              190
228 tgc gat ggc acg ctt att gtc acc gcc gcc cat ttg aca tat acc att      624
229 Cys Asp Gly Thr Leu Ile Val Thr Ala Ala His Leu Thr Tyr Thr Ile
230                               195                              200                              205
232 aat gcg ccg gag gct gcc tct ttc ctt gcg tcg aag gtt cag tca gct      672
233 Asn Ala Pro Glu Ala Ala Ser Phe Leu Ala Ser Lys Val Gln Ser Ala
234                               210                              215                              220
236 tag                                                                    675
239 <210> SEQ ID NO: 5
240 <211> LENGTH: 780
241 <212> TYPE: DNA
242 <213> ORGANISM: Aspergillus oryzae
244 <220> FEATURE:
245 <221> NAME/KEY: CDS
246 <222> LOCATION: (1)..(780)
248 <400> SEQUENCE: 5
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251 1                               5                               10                               15
253 agt cca gta gat atc cag gaa cgc cag ctc tcc ggc gga aac gag ctg      96
254 Ser Pro Val Asp Ile Gln Glu Arg Gln Leu Ser Gly Gly Asn Glu Leu
255                               20                               25                               30
257 cga gat ggc tct tgc aag ccg atc acc ttc atc ttt gcc cgc gct tcc      144
258 Arg Asp Gly Ser Cys Lys Pro Ile Thr Phe Ile Phe Ala Arg Ala Ser
259                               35                               40                               45
261 aca gag cca gga ctt ttg ggt ata tca act ggc cct gca gtc tgc aat      192
262 Thr Glu Pro Gly Leu Leu Gly Ile Ser Thr Gly Pro Ala Val Cys Asn

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```

263      50      55      60
265 ggc ttg aag atg gcc aaa gcg ggc caa gta gct tgc cag ggt gtt gga      240
266 Gly Leu Lys Met Ala Lys Ala Gly Gln Val Ala Cys Gln Gly Val Gly
267 65      70      75      80
269 ccc aag tac acg gca gac ctc gca tca aat gct ttg ccc gag aac acg      288
270 Pro Lys Tyr Thr Ala Asp Leu Ala Ser Asn Ala Leu Pro Glu Asn Thr
271      85      90      95
273 tcc cca gct gcc atc caa gag gca caa gac ctg ttc cag cag gcc gtc      336
274 Ser Pro Ala Ala Ile Gln Glu Ala Gln Asp Leu Phe Gln Gln Ala Val
275      100      105      110
277 acc aaa tgc cct gac acc caa att gtt gcc ggt ggt tat agc caa ggc      384
278 Thr Lys Cys Pro Asp Thr Gln Ile Val Ala Gly Gly Tyr Ser Gln Gly
279      115      120      125
281 aca gcc gtg atg gat gac tcc atc aag cgt cta cca gac aac gtg aaa      432
282 Thr Ala Val Met Asp Asp Ser Ile Lys Arg Leu Pro Asp Asn Val Lys
283      130      135      140
285 gag aag atc aag ggt gtc gtg ctc ttc ggc tac acc cgc aac gca cag      480
286 Glu Lys Ile Lys Gly Val Val Leu Phe Gly Tyr Thr Arg Asn Ala Gln
287 145      150      155      160
289 gaa cac ggt cag att gcc aac ttt ccc aag gac aag gtc aag gtc tac      528
290 Glu His Gly Gln Ile Ala Asn Phe Pro Lys Asp Lys Val Lys Val Tyr
291      165      170      175
293 tgt gcc gta ggc gat atg gtc tgt gac ggc acc ttg atc gtg ggg ccc      576
294 Cys Ala Val Gly Asp Met Val Cys Asp Gly Thr Leu Ile Val Gly Pro
295      180      185      190
297 gcc cat ttc act tac ctg ggt aac acc ggc gaa gca act cag ttc ttg      624
298 Ala His Phe Thr Tyr Leu Gly Asn Thr Gly Glu Ala Thr Gln Phe Leu
299      195      200      205
301 ctt ggt aag ctg agt gct tcg tct tcg tct tcg tct tca tcc ggt tct      672
302 Leu Gly Lys Leu Ser Ala Ser Ser Ser Ser Ser Ser Ser Ser Gly Ser
303      210      215      220
305 tcg gat act tcg tcc gca tca aca tcc gct gct gct gac tct tct tcg      720
306 Ser Asp Thr Ser Ser Ala Ser Thr Ser Ala Ala Asp Ser Ser Ser
307 225      230      235      240
309 tct tcg tct tct tca tcg tcg cct ttt ggg aat ctt ggt aat ctc ttt      768
310 Ser Ser Ser Ser Ser Ser Ser Pro Phe Gly Asn Leu Gly Asn Leu Phe
311      245      250      255
313 ggt gga ctc tag      780
314 Gly Gly Leu
318 <210> SEQ ID NO: 6
319 <211> LENGTH: 525
320 <212> TYPE: DNA
321 <213> ORGANISM: Aspergillus oryzae
323 <220> FEATURE:
324 <221> NAME/KEY: CDS
325 <222> LOCATION: (1)..(525)
327 <400> SEQUENCE: 6
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329 Met Leu Ala Lys His Val Leu Ala Val Leu Leu Ser Val Gly Ala Ser

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RAW SEQUENCE LISTING ERROR SUMMARY

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*FYI*  
Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:30; N Pos. 3,6,9,12,15,18

Seq#:31; N Pos. 1,4,7,10,13,16

**VERIFICATION SUMMARY**

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Input Set : A:\2006-09-28 4600-0112PUS1.txt

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L:740 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0

L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0